RAW SEQUENCE LISTING PATENT APPLICATION US/08/147,912

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1 SEQUENCE LISTING 2 3 (1) General Information: 4 5 (i) APPLICANT: WAHL, DR., GEOFFREY M. 6 O'GORMAN DR., STEPHEN V. 7 8 (ii) TITLE OF INVENTION: FLP-MEDIATED GENE MODIFICATION IN 9 MAMMALIAN CELLS, AND COMPOSITIONS AND CELLS USEFUL 10 THEREFOR 11 12 (iii) NUMBER OF SEQUENCES: 4 13 14 (iv) CORRESPONDENCE ADDRESS: 15 (A) ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK (B) STREET: 444 South Flower Street, Suite 2000 16 17 (C) CITY: Los Angeles 18 (D) STATE: CA 19 (E) COUNTRY: USA 20 (F) ZIP: 90071 21 (v) COMPUTER READABLE FORM: 22 23 (A) MEDIUM TYPE: Floppy disk 24 (B) COMPUTER: IBM PC compatible 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 27 (vi) CURRENT APPLICATION DATA: 28 29 (A) APPLICATION NUMBER: US/08/147,912 30 (B) FILING DATE: 31 (C) CLASSIFICATION: 32 33 (vii) PRIOR APPLICATION DATA: 34 (A) APPLICATION NUMBER: US 07/666,252 35 (B) FILING DATE: 08-MAR-1991 36 37 (viii) ATTORNEY/AGENT INFORMATION: 38 (A) NAME: REITER MR., STEPHEN E. 39 (B) REGISTRATION NUMBER: 31192 40 (C) REFERENCE/DOCKET NUMBER: P31 8929 41 42 (ix) TELECOMMUNICATION INFORMATION: 43 (A) TELEPHONE: (619) 535-9001 44 (B) TELEFAX: (619) 535-8949 45 46 47 (2) INFORMATION FOR SEQ ID NO:1: 48 49 (i) SEQUENCE CHARACTERISTICS: 50 (A) LENGTH: 1380 base pairs 51 (B) TYPE: nucleic acid

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64 65																	
66		(xi)	SEÇ	QUENC	CE DI	ESCR	PTIC	ON: S	SEQ :	ED NO	0:1:						
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68 60						ATA											48
69 70	Met 1	Pro	GIN	Pne	Asp 5	Ile	Leu	Cys	гÅв	10	Pro	Pro	гуя	vai	15	Val	
71	_				•												
72						AGG											96
73	Arg	Gln	Phe		Glu	Arg	Phe	Glu		Pro	Ser	Gly	Glu	-	Ile	Ala	
74 75				20					25					30			
76	тта	TGT	GCT	GCT	GAA	CTA	ACC	ТАТ	тта	TGT	TGG	ATG	ATT	ACA	CAT	AAC	144
77						Leu											
78		-	35					40		•	•		45				
79																	100
80 81						AGA											192
82	GIĀ	50	Ala	TIE	гля	Arg	55	Inc	Pne	mec	ser	60	ASII	THE	116	TIE	
83																	
84	AGC	AAT	TCG	CTG	AGT	TTC	GAT	ATT	GTC	AAT	AAA	TCA	CTC	CAG	TTT	AAA	240
85		Asn	Ser	Leu	Ser	Phe	Asp	Ile	Val	Asn		Ser	Leu	Gln	Phe	_	
86 87	65					70					75					80	
88	TAC	AAG	ACG	CAA	AAA	GCA	ACA	ATT	CTG	GAA	GCC	TCA	TTA	AAG	AAA	TTG	288
89						Ala											
90					85					90					95		
91	3 MM	aam	com	maa	CD	mmm	202	» mm	3 000	COM	ma a	m 2 m	003	C 2 2 2		C D III	226
92 93						TTT Phe											336
94				100					105		-1-	-1-	011	110	_,_		
95																	
96						GAT											384
97 98	Gln	Ser	_	Ile	Thr	Asp	Ile		Ser	Ser	Leu	Gln		Gln	Phe	Glu	
98			115					120					125				
100	TCA	TCG	GAA	GAA	GCA	GAT	AAG	GGA	AAT	AGC	CAC	AGT	AAA	AAA	ATG	CTT	432
101		Ser				Asp	Lys										
102		130					135					140					

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104						GAG											480
105 106	145	Ald	Leu	Leu	ser	Glu	GIĀ	GIU	ser	TIE	155	GIU	116	Int	GIU	160	
100	145					150					133					100	
107	מיתית	CTD	חתת	TCC	ጥጥጥ	GAG	ת א תי	እርጥ	TCC	n C n	ጥጥጥ	מסמ	מממ	מים	מממ	እ ርጥ	528
109						Glu											320
110	116	пеа	VOII	Ser	165	GIU	TYL	1111	Der	170	riie	1111	Dys	1111	175	1111	
111					103					170					1/3		
112	ጥጥል	ጥልሮ	CAA	ጥጥረ	מייני	TTC	ርሞል	CCT	አ ርጥ	ጥጥር	እ ጥር	ידעע	ጥርጥ	GGA	מממ	ጥጥር	576
113						Phe											3,0
114	204	-1-	J 1	180	204		Deu		185				O, D	190	•••		
115				100					100					1,0			
116	AGC	САТ	አ ጥጥ	AAG	AAC	GTT	CAT	CCG	444	ጥሮል	ጥጥጥ	444	тта	GTC	CAA	ממת	624
117						Val											02.
118	502		195	2,0			р	200		-		-,-	205				
119								200									
120	AAG	тат	CTG	GGA	GTA	ATA	ATC	CAG	TGT	тта	GTG	ACA	GAG	ACA	AAG	ACA	672
121						Ile											
122	-1-	210		1			215		-1-			220			-4-		
123																	
124	AGC	GTT	AGT	AGG	CAC	ATA	TAC	TTC	TTT	AGC	GCA	AGG	GGT	AGG	ATC	GAT	720
125	Ser	Val	Ser	Arq	His	Ile	Tyr	Phe	Phe	Ser	Ala	Arq	Gly	Arq	Ile	Asp	
126	225			_		230	•				235	_	-	_		240	
127																	
128	CCA	CTT	GTA	TAT	TTG	GAT	GAA	TTT	TTG	AGG	AAT	TCT	GAA	CCA	GTC	CTA	768
129	Pro	Leu	Val	Tyr	Leu	Asp	Glu	Phe	Leu	Arg	Asn	Ser	Glu	Pro	Val	Leu	
130				_	245	-				250					255		
131																	
132						ACC											816
133	Lys	Arg	Val	Asn	Arg	Thr	Gly	Asn	Ser	Ser	Ser	Asn	Lys	Gln	Glu	Tyr	
134				260					265					270			
135																	
136	CAA	TTA	TTA	AAA	GAT	AAC	TTA	GTC	AGA	TCG	TAC	AAT	AAA	GCT	TTG	AAG	864
137	Gln	Leu	Leu	Lys	Asp	Asn	Leu	Val	Arg	Ser	Tyr	Asn	Lys	Ala	Leu	Lys	
138			275					280					285				
139																	
140						TCA											912
141	Lys		Ala	Pro	Tyr	Ser		Phe	Ala	Ile	Lys		Gly	Pro	Lys	Ser	
142		290					295					300					
143																	
144						TTG											960
145		Ile	Gly	Arg	His	Leu	Met	Thr	Ser	Phe		Ser	Met	Lys	Gly		
146	305					310					315					320	
147												~~ ~		~~=	~~-		1000
148						GTT											1008
149	Thr	GIU	Leu	Thr		Val	vaı	GTÅ	Asn	_	ser	Asp	гàа	Arg		ser	
150					325					330					335		
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152 153						ACG											1056
153	MIG	val	MIG	нгg	inr	Thr	TÅL	inr	uis	GTU	TTG	Inr	wig	TIE	Pro	vab	

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159		-		a Leu	Val	Ser		Tyr	Tyr	Ala	Tyr		Pro	Ile	Ser	
160			355				360					365				
161																
162																1152
163 164 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC 165 Gln His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr 166 385 390 395 400 167 168 CCC GCA TGG AAT GGG ATA ATA TCA CAG GAG GTA CTA GAC TAC CTT TCA 169 Pro Ala Trp Asn Gly Ile Ile Ser Gln Glu Val Leu Asp Tyr Leu Ser 170 405 171 172 TCC TAC ATA AAT AGA CGC ATA TAAGTACGCA TTTAAGCATA AACACGCACT 173 Ser Tyr Ile Asn Arg Arg Ile 174 420 175 176 ATGCCGTTCT TCTCATGTAT ATATATATAC AGGCAACACG CAGATATAGG TGCGACGTGA 177 178 ACAGTGAGCT GTATGTGCGC A 1380 181 (2) INFORMATION FOR SEQ ID NO:2: 182 (i) SEQUENCE CHARACTERISTICS: 184 (B) TYPE: amino acid 185 (B) TYPE: amino acid 186 (D) TOPOLOGY: linear 187 188 (ii) MOLECULE TYPE: protein 189 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: 191 192 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val 193 1 5 10 15 194 195 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 196 20 25 30 197 198 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 199 35 40 201 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 202 50 55 60			Met Il	e Ala	Leu	_	Asp	Glu	Thr	Asn		Ile	Glu	Glu	Trp	
164 CAG CAT ATA GAA CAG CTA AAG GGT AGT GCT GAA GGA AGC ATA CGA TAC GIN His Ile Glu Gln Leu Lys Gly Ser Ala Glu Gly Ser Ile Arg Tyr 385 400		370				375					380					
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167			Ile Gl	ı Gln	Leu	Lys	Gly	Ser	Ala	Glu	Gly	Ser	Ile	Arg	_	
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171		Pro Ala	Trp As:	n Gly	Ile	Ile	Ser	Gln	Glu	Val	Leu	Asp	Tyr	Leu	Ser	
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175 176 177 178 178 179 180 181 181 (2) INFORMATION FOR SEQ ID NO:2: 182 183 (i) SEQUENCE CHARACTERISTICS: 184 (A) LENGTH: 423 amino acids 185 (B) TYPE: amino acid 186 (D) TOPOLOGY: linear 187 188 (ii) MOLECULE TYPE: protein 189 190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: 191 192 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val 193 1 5 10 15 194 195 196 197 198 199 190 190 191 191 192 193 194 195 195 196 197 198 199 190 190 191 190 191 191 191 192 193 194 195 195 196 197 198 199 190 190 191 190 191 191 191 192 193 194 195 195 196 197 198 198 199 199 190 190 191 191 191 192 193 194 195 195 196 197 198 198 199 199 199 199 190 190 190 190 191 191		Ser Tyr	Ile As	n Arg	Arg	Ile										
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179 180 181 (2) INFORMATION FOR SEQ ID NO:2: 182 183 (i) SEQUENCE CHARACTERISTICS: 184 (A) LENGTH: 423 amino acids 185 (B) TYPE: amino acid 186 (D) TOPOLOGY: linear 187 188 (ii) MOLECULE TYPE: protein 189 190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: 191 192 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val 193 1 5 10 15 194 195 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 196 20 25 30 197 198 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 199 35 40 45 200 201 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 202 203																
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181 (2) INFORMATION FOR SEQ ID NO:2: 182 183 (i) SEQUENCE CHARACTERISTICS: 184 (A) LENGTH: 423 amino acids 185 (B) TYPE: amino acid 186 (D) TOPOLOGY: linear 187 188 (ii) MOLECULE TYPE: protein 189 190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: 191 192 Met Pro Gln Phe Asp Ile Leu Cys Lys Thr Pro Pro Lys Val Leu Val 193 1 5 10 15 194 195 Arg Gln Phe Val Glu Arg Phe Glu Arg Pro Ser Gly Glu Lys Ile Ala 196 20 25 30 197 198 Leu Cys Ala Ala Glu Leu Thr Tyr Leu Cys Trp Met Ile Thr His Asn 199 35 40 45 200 201 Gly Thr Ala Ile Lys Arg Ala Thr Phe Met Ser Tyr Asn Thr Ile Ile 202 50 55 60																
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193																
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202 50 55 60 203	198 199	Leu Cys	Ala Al		Leu	Thr		Leu	Сув	Trp	Met		Thr	His	Asn	
203	198 199 200		Ala Al 35	a Glu			40		_			45				
	198 199 200 201		Ala Al 35	a Glu			40		_			45				
204 Ser Asn Ser Leu Ser Phe Asp Ile Val Asn Lys Ser Leu Gln Phe Lys	198 199 200 201 202	Gly Thr	Ala Al 35	a Glu		Ala	40		_		Tyr	45				
	198 199 200 201 202 203	Gly Thr	Ala Al 35 Ala Il	a Glu e Lys	Arg	Ala 55	40 Thr	Phe	Met	Ser	Tyr 60	45 Asn	Thr	Ile	Ile	

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205 206	65					70					75					80
207 208 209	Tyr	Lys	Thr	Gln	Lys 85	Ala	Thr	Ile	Leu	Glu 90	Ala	Ser	Leu	Lys	Lys 95	Leu
210 211 212	Ile	Pro	Ala	Trp 100	Glu	Phe	Thr	Ile	Ile 105	Pro	Tyr	Tyr	Gly	Gln 110	Lys	His
213 214 215	Gln	Ser	Asp 115	Ile	Thr	Asp	Ile	Val 120	Ser	Ser	Leu	Gln	Leu 125	Gln	Phe	Glu
216 217 218	Ser	Ser 130	Glu	Glu	Ala	Asp	Lys 135	Gly	Asn	Ser	His	Ser 140	Lys	Lys	Met	Leu
219 220 221	Lys 145	Ala	Leu	Leu	Ser	Glu 150	Gly	Glu	Ser	Ile	Trp 155	Glu	Ile	Thr	Glu	Lys 160
222 223 224	Ile	Leu	Asn	Ser	Phe 165	Glu	Tyr	Thr	Ser	Arg 170	Phe	Thr	ГÀв	Thr	Lys 175	Thr
225 226 227	Leu	Tyr	Gln	Phe 180	Leu	Phe	Leu	Ala	Thr 185	Phe	Ile	Asn	Cys	Gly 190	Arg	Phe
228 229 230	Ser	Asp	Ile 195	Lys	Asn	Val	Asp	Pro 200	ГÀв	Ser	Phe	ГÀв	Leu 205	Val	Gln	Asn
231 232 233	Lys	Tyr 210	Leu	Gly	Val	Ile	Ile 215	Gln	СЛа	Leu	Val	Thr 220	Glu	Thr	ГÀв	Thr
234 235 236	Ser 225	Val	Ser	Arg	His	11e 230	Tyr	Phe	Phe	Ser	Ala 235	Arg	Gly	Arg	Ile	Asp 240
237 238 239	Pro	Leu	Val	Tyr	Leu 245	Asp	Glu	Phe	Leu	Arg 250	Asn	Ser	Glu	Pro	Val 255	Leu
240 241 242	Lys	Arg	Val	Asn 260	Arg	Thr	Gly	Asn	Ser 265	Ser	Ser	Asn	Lys	Gln 270	Glu	Tyr
243 244 245	Gln	Leu	Leu 275	Lys	Asp	Asn	Leu	Val 280	Arg	Ser	Tyr	Asn	Lys 285	Ala	Leu	Lys
246 247 248	Lys	Asn 290	Ala	Pro	Tyr	Ser	Ile 295	Phe	Ala	Ile	ГÀв	Asn 300	Gly	Pro	Lys	Ser
249 250 251	His 305	Ile	Gly	Arg	His	Leu 310	Met	Thr	Ser	Phe	Leu 315	Ser	Met	Lys	Gly	Leu 320
252 253 254	Thr	Glu	Leu	Thr	Asn 325	Val	Val	Gly	Asn	Trp 330	Ser	Asp	Lys	Arg	Ala 335	Ser
255	Ala	Val	Ala	Arg	Thr	Thr	Tyr	Thr	His	Gln	Ile	Thr	Ala	Ile	Pro	Asp

RAW SEQUENCE LISTING PATENT APPLICATION US/08/147,912

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256				340					345	,				350				
257 258 259	His	Tyr	Phe	Ala	Leu	Val	Ser	Arg 360	Tyr	Tyr	Ala	Tyr	Asp 365	Pro	Ile	Ser		
260 261 262	Lys	Glu 370	Met	Ile	Ala	Leu	Lys 375	Asp	Glu	Thr	Asn	Pro 380	Ile	Glu	Glu	Trp		
263 264			Ile	Glu	Gln			Gly	Ser	Ala			Ser	Ile	Arg	_		
265 266	385					390					395		_	_	_	400		
267 268 269	Pro	Ala	Trp	Asn	Gly 405	Ile	Ile	Ser	Gln	Glu 410		Leu	Asp	Tyr	Leu 415	Ser		
270 271 272	Ser	Tyr	Ile	Asn 420	Arg	Arg	Ile											
272 273 274	(2)	INF	ORMA!	rion	FOR	SEQ	ID I	10:3	:									
275		(i) SE															
276				A) LI														
277 278			•	B) Ti														
279	(C) STRANDEDNESS: unknown (D) TOPOLOGY: unknown																	
280																		
281		(ii) MOI	LECU	LE T	PE:	CDN	A										
282							_											
283 284		(AT	OR:	C) II				יית א זר	. 10°1	T D ~	a a a mi	ainai	-ion	+ = =	not (-i+a		
285			(,	C) I	ADIA.	LDUA	2 130	JUNI	e: F	LP I	ecoiii	JIIIa	.1011	car	get :	3166		
286																		
287		(xi) SE	QUEN	CE DI	ESCR	IPTI	ON:	SEQ :	ID NO	0:3:							
288																		
289	GAA	GTTC	CTA :	TTCT	CTAG	AA AA	STAT	AGGA	A CT	rc							34	
290		***	001131	77011	202	270	* .											
291 292	(2)	INF	ORMA'	LION	FOR	SEQ	ו טו	NO: 4	:									
293		(i) SE	OUEN	CE CI	HARAG	TTER	ISTI	cs:									
294		(-	•	A) L														
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302		,		C) II				OLAT	E: S	ynthe	etic	oli	gonu	cleo	tide			
303			•	•					•				-					
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305 306		(xi) SE	QUEN	CE DI	ESCR:	IPTI	ON:	SEQ :	ID NO	0:4:							
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	GATCCCGGGC	TACCATGGAG	AAGTTCCTAT	TCCGAAGTTC	CTATTCTCTA	GAAAGTATAG	60
308 309	GAACTTCA						68
310	GAACIICA						00

SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/147,912

DATE: 01/07/94 TIME: 14:50:11

INPUT SET: S811.raw

Line Error

Original Text

SEQUENCE MISSING ITEM REPORT PATENT APPLICATION US/08/147,912

DATE: 01/07/94 TIME: 14:50:11

INPUT SET: S811.raw

< < THERE ARE NO ITEMS MISSING >>

SEQUENCE CORRECTION REPORT PATENT APPLICATION US/08/147,912

DATE: 01/07/94 TIME: 14:50:12

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Corrected Text